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Of 10 Inteligenetics  
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FastDB - Fast Pairwise Comparison of Sequences  
Release 5.4

Results file seqid14vs27and28.res made by spaul on Fri 15 Aug 103 7:52:05-PDT.

Query sequence being compared: US-09-581-252-14 (1-353)  
Number of sequences searched: 6  
Number of scores above cutoff: 6

Results of the initial comparison of US-09-581-252-14 (1-353) with:  
File: US09581252.pep

100-  
-  
-  
50-  
-  
-  
B  
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-  
E  
-  
-  
R  
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-  
O  
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F 10-  
-  
S  
-  
E 5-  
-  
Q  
-  
U  
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V  
-  
E  
-  
N  
-  
C  
-  
E  
-  
S  
-  
0  
-----  
SCORE 0 39 78 118 157 196 235 275 314 353  
STDEV -4 -3 -2 -1 0  
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PARAMETERS  
Similarity matrix PAM-150 K-tuple 2  
Threshold level of sim. 16%  
Mismatch penalty 1 Joining penalty 20  
P penalty 5.00 Window size 353  
P size penalty 0.05  
Cutoff score 1  
Randomization group 0

SEARCH STATISTICS

Scores: Mean 321 Median 353 Standard Deviation 60.62  
Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00  
Number of residues: 1979  
Number of sequences searched: 6  
Number of scores above cutoff: 6

The scores below are sorted by initial score.  
Significance is calculated based on initial score.

2 100% identical sequences to the query sequence were found:

Sequence Name	Description	Init. Opt.	Length	Score	Score	Sig.	Frame
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1. US-09-581-252-29 Sequence 29, Application 353 353 353 0.53 0  
2. US-09-581-252-14 Sequence 14, Application 353 353 353 0.53 0  
The list of other best scores is:

Sequence Name	Description	Length	Score	Score	Sig.	Frame
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1. US-09-581-252-14 (1-353)  
US-09-581-252-29 Sequence 29, Application US/09581252  
Initial Score = 353 Optimized score = 353 Significance = 0.53  
Residue Identity = 100% Matches = 353 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

X 10 20 30 40 50 60 70  
MNECHYDKHMDFFYNSRNTDVTDDMTGKLVIVLCVGTFFCLFIFFSNSLVIAAVINRKRFFHFFYYLLANL  
MNECHYDKHMDFFYNSRNTDVTDDMTGKLVIVLCVGTFFCLFIFFSNSLVIAAVINRKRFFHFFYYLLANL  
X 10 20 30 40 50 60 70  
MNECHYDKHMDFFYNSRNTDVTDDMTGKLVIVLCVGTFFCLFIFFSNSLVIAAVINRKRFFHFFYYLLANL

AAADFFAGIAYVFLMFNTGVSCKTLTVNRMFLRQGLDSSLTSLTLVIAVERHNSIMRMVHSLTKKR  
AAADFFAGIAYVFLMFNTGVSCKTLTVNRMFLRQGLDSSLTSLTLVIAVERHNSIMRMVHSLTKKR  
AAADFFAGIAYVFLMFNTGVSCKTLTVNRMFLRQGLDSSLTSLTLVIAVERHNSIMRMVHSLTKKR  
X 80 90 100 110 120 130 140

VTLLILLVMAIAIFMGAVPTLGMNCLNISACSLAPIYSRSYVFTVSNLMAFLMNVYLLIYVYVKK  
VTLLILLVMAIAIFMGAVPTLGMNCLNISACSLAPIYSRSYVFTVSNLMAFLMNVYLLIYVYVKK  
VTLLILLVMAIAIFMGAVPTLGMNCLNISACSLAPIYSRSYVFTVSNLMAFLMNVYLLIYVYVKK  
X 150 160 170 180 190 200 210

TNVLSPHTSGSISRRTPMKLMKTVMTVLGAFVYCGTLPGLVYVLPDLGNCRCQGVQYHKKRFFLLALLNSV  
TNVLSPHTSGSISRRTPMKLMKTVMTVLGAFVYCGTLPGLVYVLPDLGNCRCQGVQYHKKRFFLLALLNSV  
TNVLSPHTSGSISRRTPMKLMKTVMTVLGAFVYCGTLPGLVYVLPDLGNCRCQGVQYHKKRFFLLALLNSV  
X 220 230 240 250 260 270 280

290 300 310 320 330 340 350 X  
NPIIYSYKDEDMYGTMKMKTCFSGQENPERPSRIPSTVLSRSDTGSQYIEDSISOGAVCNKSTS  
NPIIYSYKDEDMYGTMKMKTCFSGQENPERPSRIPSTVLSRSDTGSQYIEDSISOGAVCNKSTS  
NPIIYSYKDEDMYGTMKMKTCFSGQENPERPSRIPSTVLSRSDTGSQYIEDSISOGAVCNKSTS  
X 290 300 310 320 330 340 350 X

2. US-09-581-252-14 (1-353)  
US-09-581-252-14 Sequence 14, Application US/09581252  
Initial Score = 353 Optimized score = 353 Significance = 0.53  
Residue Identity = 100% Matches = 353 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

X 10 20 30 40 50 60 70  
MNECHYDKHMDFFYNSRNTDVTDDMTGKLVIVLCVGTFFCLFIFFSNSLVIAAVINRKRFFHFFYYLLANL  
MNECHYDKHMDFFYNSRNTDVTDDMTGKLVIVLCVGTFFCLFIFFSNSLVIAAVINRKRFFHFFYYLLANL  
MNECHYDKHMDFFYNSRNTDVTDDMTGKLVIVLCVGTFFCLFIFFSNSLVIAAVINRKRFFHFFYYLLANL  
X 10 20 30 40 50 60 70

AAADFFAGIAYVFLMFNTGVSCKTLTVNRMFLRQGLDSSLTSLTLVIAVERHNSIMRMVHSLTKKR  
AAADFFAGIAYVFLMFNTGVSCKTLTVNRMFLRQGLDSSLTSLTLVIAVERHNSIMRMVHSLTKKR  
AAADFFAGIAYVFLMFNTGVSCKTLTVNRMFLRQGLDSSLTSLTLVIAVERHNSIMRMVHSLTKKR  
X 80 90 100 110 120 130 140

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150      160      170      180      190      200      210
VTLLLLVMAIAIFPGAVPTLGAMNCLNISACSSLAIPYSSTYLEFWTSNLMFLIMVVYLRIVYVKRR
150      160      170      180      190      200      210
VTLLILLVMAIAIFMGAVPTLGAMNCLNISACSSLAIPYSSTYLEFWTSNLMFLIMVVYLRIVYVKRR
220      230      240      250      260      270      280
TNVLSPTSGSISRRTPMKIMKTVMYVLGAFVYVCWMPGLVVLPLDGLNCRQCGVQHVKRMFLALLNSVY
220      230      240      250      260      270      280
TNVLSPTSGSISRRTPMKIMKTVMYVLGAFVYVCWMPGLVVLPLDGLNCRQCGVQHVKRMFLALLNSVY
290      300      310      320      330      340      350      X
NPILSYKXDEDMYCTMKMKMICFSQENBERPSPRIPTVLSRDTGSOYIEDSISQGAVCKNKT
290      300      310      320      330      340      350      X
NPILSYKXDEDMYCTMKMKMICFSQENBERPSPRIPTVLSRDTGSOYIEDSISQGAVCKNKT

```

[illegible]

Initial Score	=	352	Optimized Score	=	352	Significance	=	0.51
Residue Identity	=	99%	Matches	=	351	Mismatches	=	2
Gaps	=	0	Conservative Substitutions	=			=	0

5. US-09-581-252-14 (1-353)  
US-09-581-252-23 Sequence 23, Application US/09581252

[illegible]

	Gaps	-	1	Conservative	Substitutions	-	8
X	10	20	30	40	50	60	70
MNECHYDKHMOPEFYNRSTVDVDMGTGKLIYIVLCVGTFCFLTFEFSNLSVIAAVIKNRKHPPEYLLANL							
MNECHYDKRMOPFYNRSTVDPADEMTGKLIYIVLCVGTFCFLTFEFSNLSVIAAVITRKHPPEYLLANL							
X	10	20	30	40	50	60	70
AADEPFAIAIVFLMFNNGPVSKITLVNRMLFROGLDSSLTASTLNLIYAVENHMSIMRMRYHSNTTKRK							
80	90	100	110	120	130	140	
AADEPFAIAIVFLMFNNGPVSKITLVNRMLFROGLDSSLTASTLNLIYAVENHMSIMRMRYHSNTTKRK							
AADEPFAIAIVFLMFNNGPVSKITLVNRMLFROGLDSSLTASTLNLIYAVENHMSIMRMRYHSNTTKRK							
80	90	100	110	120	130	140	
VTLLILLYMAIAIFMGAPVTLGWNCLICISACSSISAPYLSRYLTFMWNSLLAFETINAVYRIVRYMKVKKRK							
150	160	170	180	190	200	210	
VTLLILLYMAIAIFMGAPVTLGWNCLICISACSSISAPYLSRYLTFMWNSLLAFETINAVYRIVRYMKVKKRK							
150	160	170	180	190	200	210	
VTLLILLYMAIAIFMGAPVTLGWNCLICISACSSISAPYLSRYLTFMWNSLLAFETINAVYRIVRYMKVKKRK							
150	160	170	180	190	200	210	
TNVLSPHTSGISISRRRTPMKLMKTYMTVLGAFVYVCWTPGLVYLPDGLNCRQCGQVQHVKRMFLLLALNSVY							
220	230	240	250	260	270	280	
TNVLSPHTSGISISRRRTPMKLMKTYMTVLGAFVYVCWTPGLVYLPDGLNCRQCGQVQHVKRMFLLLALNSVY							
TNVLSPHTSGISISRRRTPMKLMKTYMTVLGAFVYVCWTPGLVYLPDGLNCRQCGQVQHVKRMFLLLALNSVY							
220	230	240	250	260	270	280	
NPIIYSYKDEDMYGTMKMKMICCFSEF-NPERRPSRISTVLSRSDTSGQYIETDISOGAVCNKST							
150	160	170	180	190	200	210	
NPIIYSYKDEDMYGTMKMKMICCFSEF-NPERRPSRISTVLSRSDTSGQYIETDISOGAVCNKST							
150	160	170	180	190	200	210	
NPIIYSYKDEDMYGTMKMKMICCFSEF-NPERRPSRISTVLSRSDTSGQYIETDISOGAVCNKST							
150	160	170	180	190	200	210	
NPIIYSYKDEDMYGTMKMKMICCFSEF-NPERRPSRISTVLSRSDTSGQYIETDISOGAVCNKST							
150	160	170	180	190	200	210	
NPIIYSYKDEDMYGTMKMKMICCFSEF-NPERRPSRISTVLSRSDTSGQYIETDISOGAVCNKST							
150	160	170	180	190	200	210	
NPIIYSYKDEDMYGTMKMKMICCFSEF-NPERRPSRISTVLSRSDTSGQYIETDISOGAVCNKST							
150	160	170	180	190	200	210	
NPIIYSYKDEDMYGTMKMKMICCFSEF-NPERRPSRISTVLSRSDTSGQYIETDISOGAVCNKST							
150	160	170	180	190	200	210	
NPIIYSYKDEDMYGTMKMKMICCFSEF-NPERRPSRISTVLSRSDTSGQYIETDISOGAVCNKST							
150	160	170	180	190	200	210	
NPIIYSYKDEDMYGTMKMKMICCFSEF-NPERRPSRISTVLSRSDTSGQYIETDISOGAVCNKST							
150	160	170	180	190	200	210	
NPIIYSYKDEDMYGTMKMKMICCFSEF-NPERRPSRISTVLSRSDTSGQYIETDISOGAVCNKST							
150	160	170	180	190	200	210	
NPIIYSYKDEDMYGTMKMKMICCFSEF-NPERRPSRISTVLSRSDTSGQYIETDISOGAVCNKST							
150	160	170	180	190	200	210	
NPIIYSYKDEDMYGTMKMKMICCFSEF-NPERRPSRISTVLSRSDTSGQYIETDISOGAVCNKST							
150	160	170	180	190	200	210	
NPIIYSYKDEDMYGTMKMKMICCFSEF-NPERRPSRISTVLSRSDTSGQYIETDISOGAVCNKST							
150	160	170	180	190	200	210	
NPIIYSYKDEDMYGTMKMKMICCFSEF-NPERRPSRISTVLSRSDTSGQYIETDISOGAVCNKST							
150	160	170	180	190	200	210	
NPIIYSYKDEDMYGTMKMKMICCFSEF-NPERRPSRISTVLSRSDTSGQYIETDISOGAVCNKST							
150	160	170	180	190	200	210	
NPIIYSYKDEDMYGTMKMKMICCFSEF-NPERRPSRISTVLSRSDTSGQYIETDISOGAVCNKST							
150	160	170	180	190	200	210	
NPIIYSYKDEDMYGTMKMKMICCFSEF-NPERRPSRISTVLSRSDTSGQYIETDISOGAVCNKST							
150	160	170	180	190	200	210	

Initial Score	-	352	Optimized Score	-	352	Significance	-	0.51
Residue Identity	-	99%	Matches	-	332	Mismatches	-	1
Gaps	-	0	Conservative Substitutions	-			-	0

  

X	.10	20	30	40	50	60	70
MNECHYDKHDFNRSNTDPTDMDTGTKLYLVLCVGFPCCLFFESNSLVAIVIKNRKRFHPFYLLAL							
MNECHDKHDFNRSNTDPTDMDTGTKLYLVLCVGFPCCLFFESNSLVAIVIKNRKRFHPFYLLAL							
X	10	20	30	40	50	60	70
AAADFFGIAIVYFLMFTGVSCKLYIVNRNPLRQGLDSSILTASLIVLVAIERRHNSIMRVRHSLDTKKR							

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6. US-09-581-252-14 (1-353)
   US-09-581-252-15 Sequence 15, Application US/09581252

Initial Score      = 201 Optimized score = 202 Significance = -1.98
Residue Identity  = 89% Matches          = 190 Mismatches   = 20
Caps              = 0 Conservative Substitutions

40      50      60      70      80      90      100      110
FFCLFFFSNLSVIAAVIKKKHFPPYLLANLAADFAGIAYVLFMFVGTGVSKTLLVNNRFLRGGD
|||||
NTGFSKTLTVNNRFLRGGD
X      10      20

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40      50      60      70      80      90     100     110
FECLPFFSNSLVIAAVIKNRKFFHPFYLLANLAADFFAGIAYVFLMFNTGVPYSKTLTVNRWFLROGLD
|||||
NTGVPYSKTLTVNRWFLROGLD
X      10      20

120      130      140      150      160      170      180
SSLTSLTNLLVIAVERHMSIMRMFVHSNLTTRKRYTLTLILVMAIAIFMGAVPTLGWNCICNISACSSLAPI
|||||
TSLFASLANLVIAVERHMSIMRMFVHSNLTTRKRYTLTLILVMAIAIFMGAVPTLGWNCICNISACSSLAPI
30      40      50      60      70      80      90

190      200      210      220      230      240      250
YRSRYLVFWTVSNLMAFLIMVYVLRIVYVYKRTNVLSPHTSGSISRRTPMKLMKTYMTVLGAFVYCWTP
|||||
YRSRYLVFWTVSNLMAFLIMVYVLRIVYVYKRTNVLSPHTSGSISRRTPMKLMKTYMTVLGAFVYCWTP
100      110      120      130      140      150      160

260      270      280      290      300      310      320
GLVYVLLDGLNCRQCGVOHVKKRWFLLALNSVNPILITYSKDEDMYGTMMKKMICCFSEQENPERRPSRIPST
|||||
GLVYVLLDGLNCRQCGVOHVKKRWFLLALNSVNPILITYSKDEDMYGTMMKKMICCFSEQENPERRPSRIPST
170      180      190      200      210 X

330      340      350
VLSRSDTGSQYIEDSISQGAVCNKS

```

Sequence Name	Description	Length	Score	Score	Seq. Frame
			Init.	Opt.	

X 20 30 40 50 60 70  
MNECHYKHNDEFFYNRSNPTDMDGTGKLVLCGTFECFLPIFESNLSLVAAYIKNRKHFPPYYLLANL  
MNECHYKHNDEFFYNRSNPTDMDGTGKLVLCGTFECFLPIFESNLSLVAAYIKNRKHFPPYYLLANL  
MNECHYKHNDEFFYNRSNPTDMDGTGKLVLCGTFECFLPIFESNLSLVAAYIKNRKHFPPYYLLANL  
X 10 20 30 40 50 60 70  
MNECHYKHNDEFFYNRSNPTDMDGTGKLVLCGTFECFLPIFESNLSLVAAYIKNRKHFPPYYLLANL

Initial Score	-	352	Optimized score	-	352	Significance	-	0.51
Residue Identity	-	99%	Matches	-	352	Mismatches	-	1
Gaps	-	0	Conservative Substitutions	-			-	0

  

X	10	20	30	40	50	60	70
MNECHYDKHMEFFYNRSNTDIPVDMTGKTLVLCVGTFFCLFIFFSNSLIVANAIVKRNKRKHFFPYLLANL							

Initial Score	-	202	Optimized score	-	203	Significance	-	-1.98
Residue Identity	-	898	Matches	-	191	Mismatches	-	19
Gaps	-	0	Conservative Substitutions	-			-	3

```
120 130 140 150 160 170 180
SSLTASLTNLLVIAVERHMSIMRMRVHSNLTFRKRYTLTLVWAIATFEMGAVPTLGMNCLCNISACSSLAPI
|||||
TSLTASLTNLLVIAVERHMSIMRMRVHSNLTFRKRYTLTLVWAIATFEMGAVPTLGMNCLCNISACSSLAPI
30 40 50 60 70 80 90
190 200 210 220 230 240 250
YRSYLVFWTVSNLMAFLIMVVYLRIYVYVKRKTNVLSPHTSGSISRRRTPMKLTVMTVLGAFFVVCWTP
|||||
YRSYLVFWTVSNLMAFLIMVVYLRIYVYVKRKTNVLSPHTSGSISRRRTPMKLTVMTVLGAFFVVCWTP
100 110 120 130 140 150 160
GLVYVLPDGLNCRCQGVQHVKKRMFLLLALLNSVNPPIYSYKDEDMYGTMKKMKCCFSQENPERRRSRIPST
|||||
GLVYVLPDGLNCRCQGVQHVKKRMFLLLALLNSVNPPIYSYKDEDMYGTMKKMKCCFSQENPERRRSRIPST
170 180 190 200 210 X
330 340 350
VLSRSDTGSQYIEDSISQGAVCNKS
```